

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bednarik, Daniel P.
Olsen, Henrik S.
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(ii) TITLE OF INVENTION: Soluble Interleukin-1 Receptor Accessory Molecule

(iii) NUMBER OF SEQUENCES: 30

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/024,581
(B) FILING DATE: 26-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1488.0450001/EKS/KMT

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 303..1370

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 303..353

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 354..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGTGGCGCC CGTTCTAGAA CTAGTGGATC CCCCCGGGATG CAGGAATTG	GCACGAGAAA	60
GTGCGGCGGA AAGTAAGAGG CTCACTGGGG AAGACTGCCG GGATCCAGGT	CTCCGGGGTC	120
CGCTTTGGCC AGAGGCGCGG AAGGAAGCAG TGCCCGGCGA CACTGCACCC	ATCCCGGCTG	180
CTTTTGCTGC GCCCTCTCAG CTTCCCAAGA AAGGCATCGT CATGTGATCA	TCACCTAAGA	240
ACTAGAACAT CAGCAGGCC CTTAGAAGCCT CACTCTTGCC CCTCCCTTTA	ATATCTCAAA	300
GG ATG ACA CTT CTG TGG TGT GTA GTG AGT CTC TAC TTT TAT	GGA ATC	347
Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile		
-17 -15 -10 -5		
CTG CAA AGT GAT GCC TCA GAA CGC TGC GAT GAC TGG GGA CTA GAC	ACC	395
Leu Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr		
1 5 10		
ATG AGG CAA ATC CAA GTG TTT GAA GAT GAG CCA GCT CGC ATC AAG	TGC	443
Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys		
15 20 25 30		
CCA CTC TTT GAA CAC TTC TTG AAA TTC AAC TAC AGC ACA GCC CAT TCA		491
Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser		
35 40 45		
GCT GGC CTT ACT CTG ATC TGG TAT TGG ACT AAG CAG GAC CGG GAC CTT		539
Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Lys Gln Asp Arg Asp Leu		
50 55 60		
GAG GAG CCA ATT AAC TTC CGC CTC CCC GAG AAC CGC ATT AGT AAG GAG		587
Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu		
65 70 75		
AAA GAT GTG CTG TGG TTC CGG CCC ACT CTC CTC AAT GAC ACT GGC AAC		635
Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn		
80 85 90		
TAT ACC TGC ATG TTA AGG AAC ACT ACA TAT TGC AGC AAA GTT GCA TTT		683

Tyr Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe			
95	100	105	110
CCC TTG GAA GTT GTT CAA AAA GAC AGC TGT TTC AAT TCC CCC ATG AAA			731
Pro Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys			
115	120	125	
CTC CCA GTG CAT AAA CTG TAT ATA GAA TAT GGC ATT CAG AGG ATC ACT			779
Leu Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr			
130	135	140	
TGT CCA AAT GTA GAT GGA TAT TTT CCT TCC AGT GTC AAA CCG ACT ATC			827
Cys Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile			
145	150	155	
ACT TGG TAT ATG GGC TGT TAT AAA ATA CAG AAT TTT AAT AAT GTA ATA			875
Thr Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile			
160	165	170	
CCC GAA GGT ATG AAC TTG AGT TTC CTC ATT GCC TTA ATT TCA AAT AAT			923
Pro Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn			
175	180	185	190
GGA AAT TAC ACA TGT GTT ACA TAT CCA GAA AAT GGA CGT ACG TTT			971
Gly Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe			
195	200	205	
CAT CTC ACC AGG ACT CTG ACT GTA AAG GTA GTC TCT CCA AAA AAT			1019
His Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn			
210	215	220	
GCA GTG CCC CCT GTG ATC CAT TCA CCT AAT GAT CAT GTG GTC TAT GAG			1067
Ala Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu			
225	230	235	
AAA GAA CCA GGA GAG GAG CTA CTC ATT CCC TGT ACG GTC TAT TTT AGT			1115
Lys Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser			
240	245	250	
TTT CTG ATG GAT TCT CGC AAT GAG GTT TGG TGG ACC ATT GAT GGA AAA			1163
Phe Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys			
255	260	265	270
AAA CCT GAT GAC ATC ACT ATT GAT GTC ACC ATT AAC GAA AGT ATA AGT			1211
Lys Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser			
275	280	285	
CAT AGT AGA ACA GAA GAT GAA ACT AGA ACT CAG ATT TTG AGC ATC AAG			1259
His Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys			
290	295	300	
AAA GTT ACC TCT GAG GAT CTC AAG CGC AGC TAT GTC TGT CAT GCT AGA			1307
Lys Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg			
305	310	315	

AGT GCC AAA GGC GAA GTT GCC AAA GCA GCC AAG GTG AAG CAG AAA GGT	1355	
Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Gly		
320	325	330
AAT AGA TGC GGT CAG TGATGAATCT CTCAGCTCCA AATTAACATT GTGGTGAATA	1410	
Asn Arg Cys Gly Gln		
335		
AGGACAAAAG GAGAGATTGA GAACAAGAGA GCTCCAGCAC CTAGCCTGAC GGCATCTAAC	1470	
CCATAGTAAT GAATCAAAC TAAATGAAAA ATATGAAAGT TTTCATCTAT GTAAGATACT	1530	
CAAAATATTG TTTCTGATAT TGTTAGTACC GTAATGCCA AATGTAGCTA AAAAAATCGA	1590	
CGTGAGTACA GTGAGACACA ATTTTGTGTC TGTACAATT TGAAAAATT AAAACAAAGA	1650	
AAATATTCAA AGCTACAAA GATAGAAAA ACTGGTAGAG CCACATATTG TTGGTGAATT	1710	
ATTAAGACCC TTTTAAAAAT CATTCACTGGT AGAGTTAAG AGTCATAAAA AAGATTGCAT	1770	
CATCTGACCT AAGACTTTCG GAATTTTCC TGAACAAATA ACAGAAAGGG AATTATATAC	1830	
CTTTTAATAT TATTAGAAC ATTATCTGTA GTTGTAAAAC ATTATTAATA GCAGCCATCC	1890	
AATTGTATGC AACTAATTAA GGTATTGAAT GTTTATTTTC CAAAAATGCA TAATTATAAT	1950	
ATTATTTAA ACACATATGTA TCAATATTAA AGCAGGTTA TAATATACCA GCAGCCACAA	2010	
TTGCTAAAAT GAAAATCATT TAAATTATGA TTTAAATGG TATACACATG ATTTCTATGT	2070	
TGATAGTACT ATATTATTCT ACAATAAAATG GAAATTATAA AGCCTTCTTG TCAGAAGTGC	2130	
TGCTCCTAAA AAAAAAAA AAAAA	2155	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Leu	Leu	Trp	Cys	Val	Val	Ser	Leu	Tyr	Phe	Tyr	Gly	Ile	Leu
-17	-15														-5
Gln	Ser	Asp	Ala	Ser	Glu	Arg	Cys	Asp	Asp	Trp	Gly	Leu	Asp	Thr	Met
1					5					10					15
Arg	Gln	Ile	Gln	Val	Phe	Glu	Asp	Glu	Pro	Ala	Arg	Ile	Lys	Cys	Pro
				20				25					30		

Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
35 40 45

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Lys Gln Asp Arg Asp Leu Glu
50 55 60

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
65 70 75

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
80 85 90 95

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
100 105 110

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
115 120 125

Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
130 135 140

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
145 150 155

Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
160 165 170 175

Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
180 185 190

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
195 200 205

Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
210 215 220

Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
225 230 235

Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
240 245 250 255

Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
260 265 270

Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
275 280 285

Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
290 295 300

Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
305 310 315

Ala Lys Gly Glu Val Ala Ala Lys Val Lys Gln Lys Gly Asn

320

325

330

335

Arg Cys Gly Gln

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Leu Trp Tyr Leu Met Ser Leu Ser Phe Tyr Gly Ile Leu
1 5 10 15

Gln Ser His Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
20 25 30

Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
35 40 45

Leu Phe Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser
50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe
130 135 140

Pro Val His Lys Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr
165 170 175

Trp Tyr Lys Gly Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro
180 185 190

Glu Gly Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly
195 200 205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His
210 215 220

Leu Thr Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala
225 230 235 240

Leu Pro Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys
245 250 255

Glu Pro Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe
260 265 270

Ile Met Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
275 280 285

Pro Asp Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr
290 295 300

Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305 310 315 320

Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn
325 330 335

Thr Lys Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys
340 345 350

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTATGAGAA AGAACAAAGGA GAGGAGCTAC TCATTCCCTG TACGGTCTAT TTTAGTTTC	60
TGATGGATTG TCGCAATGAG GTTTGGTGGA CCATTGATGG AAAAAAACCT GATGACATCA	120
CTATTGATGT CACCATTAAC GAAAGTATAA GTCATAGTAG AACAGAAGAT GAAACAAGAA	180
CTCAGATTTT GAGCATCAAG AAAGTTACCT CTGAGGATCT CAAGCGCANT ANTGTCTGTC	240
ATGCTAGAAG TGCCAAAGGC GAAGTTGCCA AAGCAGCCAA GGTGAAGCAG AAAG	294

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGAACCTCC AAACATATAG AAGTAAAGAC ACAGGGCTGT TATAAAATAC AGAATTTAA	60
TAATGTAATA CCCGAAGGTA TGANCTTGAG TTTCCCTCATT GCCTTAATTT CAAATAATGG	120
AAATTACACA TGTNTTGTTA CATATCCAGA AAATGGACGT ACGTTTCATC TCACCAGGAC	180
TCTGCTCTNT AAAGGTAGTA GGCTCTCCAA AAANTGCAGT GCCCCCTGTG ATCCATTAC	240
CTAATGATCA TG	252

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGACAGCGT CTTGCTCTGT CACCTGGGCT GGAGTGCAGT GGCGAGATCT CGGCTCACTG	60
CAACCTCTGC CTCCCAGGTT CAAGCAATT TCCTGCCTCA CCCTCCTGAG TAGCTGGAT	120
TACAGGTGTA TGCCACCATG CCGGCTAATT TTTGTATTTT CTAGTAGAGA CTAGGTTCA	180
CCATGTTGGC CAGGCTGGTC TTGAACATT TTTTTTCTT TTTCTCGTGC CGAATTCCCTG	240
CAGCCCGGGG GATCCACTAG TTCTAGAGCG GCCGCCACCG CGGTGGAGCT CCAGCTTTG	300
TTCCCTTTAG TGAGGGNTAA TTTCGAGCTT GGCGTAATCA TGGTCATAGC TGTTCCGT	360
GTGAAATTGT TATCCGCTCA CAATTCACA CAACATACGA GCCGGAAGCA TAAAGTGTAA	420

AGCCT

425

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCACNNAAAGG GACAAAAGCT GGAGCTCCAC CGCGGGCNGC NCGTTCTAGA ACTAGTGGAT 60
CCCCCGGGCT GCAGGAATTC 80

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAACTAGTGG ATCCCCGGG CTGCAGGAAT TCGNCACGAG ACCANCTCAC CTTTCCCCAC 60
ACTAGCTCAN GNACAGACAG ANTGGACTAA AAATAGTTGA 100

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GNCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTGGC ACGAGGGGCT GCTCGAGCTG	60
CCAACAAACGG AGCATTGCC CCGGACCTN AGCTGACATC GTGCGTAGNC TAGGCATGNG	120
TGGTTGTTAGG GACTTACGTC TTTCTACCTN GANNCACGGT TATCACTGNC GANGTCCACC	180
CACCGGGGNT GNNCAACTTN CGGNGGAAGG TACTACNTAC TTTCAAACCC CCTAACTTGT	240
TCCTTTTTTG CAGGATCGAG TN	262

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

NTTAGTGTAC AGACACAAAA TTGTGTCTCA CTGTACTCAC GTGATTTC TTAGCTACAT	60
TTGGGCATTA CGGTACTAAC AATATCAGAA ACAATATTT GAGTATCTTA CATAGATGAA	120
AACTTTCTATA TTTTCATTT AAGTTTGATT CATTACTATG GGTTAGATGC CGTCGGNTAG	180
GTGCTGGAGC TCTCTTGTTC TCAATCTCTC CTTTGTCTT TATTCACAC AATGTTAATT	240
TGGAGCTGAG AGATTCACTCA CTGACCGCAT CTATTACCTT TCTGCTTCAC CTTGGCTGCT	300
TTGGCAACTT CGCCTTGGA CCTTCTAGCA TGACAGACAT AGCTGCGCTT GAGATCCTCA	360
GAGGTAACCTT TCTTGANGCT CAAAATCTGA GTTCTTGTCTT C	401

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATAATTGTA CAGACACAAAA ATTGTGTCTC ACTGTACTCA CGTCGATTTC TTTAGCTACA	60
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TTTGGGCATT ACGGTACTAA CAATATCAGA AACAAATATT TGAGTATCTT ACATAGATGA	120
AAACTTTCAT ATTTTCATT TAAGTTTNGA TTCATTACTA TGGGTTAGAT GCCGTCGGGC	180
TNAGGTGCTG GAGCTCTCTT GTTCTCAATC TCTCCTTTG TCCTTATTCA CCACAATGTT	240
AATTTGGAGC TGAGAGATTC ATCACTGACC GCATCTATTA CCTTCTGCT TCACCTGGC	300
TCGCTTGCG AACTTCGCCT TTGGACTTCT AGCATGACAG ACATAGCTGC GCTTGGAGAT	360
CCTCAGAGGT AACTTTCTTG ATGGCTAAA ATCNGAGTTC TTGTTTCATC TTCTGTTCTA	420
CTATGACTTA TACTTTCGTT AAN	443

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CATAATTGTA CAGACACAAA ATTGTGCTCA CTGTACNCAC GTCGATTTT TTAGCTACAT	60
TTGGGCATTA CGGTACTAAC AATATCAGAA ACAATATTGTT GAGTATCTTA CATAGATGAA	120
AACTTTCATTA TTTTCATTT AAGTTGATT CATTACTATG GGTTAGATGC CGTCGGGCTA	180
GGGGCTGGAG CTCTCTTGTGTT CTCAATCTCT CCTTTGTCC TTATTACCA CAATGTTAAT	240
TTGGNGCTGA GAGATTTCATC ACTGACCGCA TCTATTACCN TTCTGCTTCA NCTTGGCTGC	300
TTGGNAACT TCGNCTTTG	319

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCTATGAGAA AGAACCAAGGA GAGGAGCTAC TCATTCCCTG TACGGTCTAT TTTAGTTTC	60
TGATGGATTC TCGCAATGAG GTTTGGTGGA CCATTGATGG AAAAAAAACCT GATGACATCA	120
CTATTGATGT CACCATTAAC GAAAGTATAA GTCATAGTAG AACAGAAGAT GAAACAAGAA	180
CTCAGATTT GAGCATCAAG AAAGTTACCT CTGAGGATCT CAAGCGCANT ANTGTCTGTC	240
ATGCTAGAAG TGCCAAAGGC GAAGTTGCCA AAGCAGCCAA GGTGAAGCAG AAAGTGCCAG	300
CTCCAAGATA CACAGTGGAA CTGGCTTGTG GTTTGGAGC CACAGTCCTG CTAGTGGTGA	360
TTCTCATTGT TGTTTACCAT GTTTACTTGG CTAGAG	396

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTCTCCAAA AAATGCAGTG CCCCTGTGA TCCATTCAACC TAATGATCAT GTGGTCTATG	60
AGAAAGAACCC AGGAGAGGAG CTACTCATTC CCTGTACGGT CTATTTAGT TTTCTGATGG	120
ATTCTCGCAA TGAGGTTGG TGGACCATTG ATGGAAAAAA ACCTGATGAC ATCACTATTG	180
ATGTCACCAT TAACGAAAGT ATAAGTCATA GTAGAACAGA AGATGAAACA AGAAACTCAGA	240
TTTGAGGCA TCAAGAAAGT TACCTCTGAG GATCTCAAGC GCNTAATNGT CTGTNCATGG	300
CTAGGAAGTG CCAAAGNGGA AGTTGGCCAA AGGCAGCCAA GGTNGAGGCA GGAAAGGTTA	360
TTAGGTGGCG GTTCAGTTGA TGGATTCTCT TCAGGNTCCC AATTTAACN TTGTTGGGTG	420
GATTAA	426

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCGGCACAG GGAACCTCCA AACATATAGA AGTAAAGACA CAGGGCTGTT ATAAAATACA	60
GAATTTTAAT AATGTAATAC CCGAAGTATG AACTTGAGTT TCCTCATTGC CTTAATTCA	120
AATAATGGAA ATTACACATG TGTTGTTACA TATCCAGAAA ATGGACGTAC GTTTCATCTC	180
ACCAGGACTC TGACTGTAAA GGTAGTAGGC TCTCCAAAAA ATGCAGTGCC CCCTGTGATC	240
CATTACACCTA ATGATCATGT GGTCTATGAG AAAGAACAG GGAGAGTAGC TACTCATTCC	300
CTGTACGGTC TATTTAGTT TTCTGATGGA TTCTCGCAAT GGAGGTTTNG TGGGACCATT	360
TGATGGGAAA AAAACCTGGA TNGACATCAN TATTTGATGT TCACCAATTAA CGGAAAGTA	420
TTAAGTCCTT AGTTAGGANC AGGTGGTTGA ANACAGGAAN TCCGGTTTTT GAGGCTTCAG	480
GAAAGTTTAC CCCTGNGGGT TCTTCAGGNG CCGATTGTTN TGTCNTTGT TNGGAGGTGN	540
CCCAGNGGAA GTTTGNCCA AGGCAGGCCAG	570

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAGTACTATC AACATAGAAA NCATGTTTAT ACCATTAAA ATCATAATT AAATGATTT	60
CATTTTAGCA ATTGTGGCTG CTGGTATATT ATAAACCTGC TTAAATATTG ATACATAGTG	120
TTTAANATAA TATTATAATT CTGCATTTT GGAAAATAAA CATTCAATAC CTTAATTAGT	180
TGCATACAAT TGGATGGCTG CTATTAATAA NGTTTACAA CTACAGATAA TGCTTCTAAT	240
ANTATTANCG GGNATA	256

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAACAGAAGA TGAAACAAGA ACTCAGATT TGAGCATCAA GAAAGTTACC TCTGAGGATC	60
TCAAGCGCAN TATTGTCTGT CATGCTAGAA GTGCCAAAGG GAANGTTGCC AAAGCAGCCA	120
AGGTGAAGCA GAAAGGTAAT AGATGCGGTC AGTGATGAAT CTCTCAGCTC CAAATTAACA	180
TTGTGGGTGA ATAAGGACAA AAGGAGAGAT TGAGGAACAA GAGAGCTCCA GCACCTAGCC	240
TGACGGCATC TTAACCCAT AGTAATTGAA TCCAACTTA AATGGAAAAN TTTGNAGTTT	300
TTTCATCCTT NGGTAGGGTA CTTCAANTTT TGT	333

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCTGACAAG AAGGCTTTAT AATTTCATT TATTGTAGAA TAATATAGTA CTATCAACAT	60
AGAAATCATG TGTATACCAT TTAAAATCAT AATTAAATG ATTTTCATT TAGCAATTGT	120
GGCTGCTGGG ATATTATAAA CCTGCTAAA TATTGATACA TAGNGTTAA AATAATATTA	180
TAATTATGCA NTTTGAAA AATAAACATT CAATACCCNT AATAGGTGCA TACAATTGGG	240
AGGGCTGCNA TTAATAATGG TTTCCACNAC C	271

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TATTTTCCAA AAATGCATAA TTATAATATT ATTTYAMMCA CTATGTATCA ATATTTAAGC	60
AGGTTTATAA TATACCAGCA GCCACAATTG CTAAAATGAA AATCATTAA ATTATGATT	120
TAAATGGTAT ACACATGATT YCTATGTTGA TAGTACTATA TTATTCTACA ATAAATGGAA	180
ATTATAACGC CTTCTTGTCA GAAAGTGCCTGC TCCT	214

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCTTTATAAT ATTTTANTTA TTGTAGAATA ATATAGTACT ATCAACATAG AAATCATGTG	60
TATACCATTT AAAATCATAA TTTAAATGAT TTTCATTAA GCAATTGTGG CTGCTGGGTA	120
TATTATAAAC CTGCTTAAAT ATTGATACAT AGTGTAAATA ATAATATTAT AATTATGGCA	180
TTTTTGGGAA ATAAACATTC AATACCTAA TTGGNTGGCA TACAATGGGG TGGGCNGGCT	240
ATTAATAATG GTTTTACAAC TACAGGGTAA TGGCNTCCTA ATAATATTAA AGGGGGGNTA	300
TAATTCCCC	309

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGNGTCCG CTTTGGCCAG ANGTNGGAAG GAAGCAGTGC CCGGCGACAC TCCACCCATC	60
CCGGCTGCTT TTGCTGCGCC CTCTCAGCTT CCCAAGAAAG GATGACACTT CTGTGGTGTG	120
TAGTGAGTCT CTACTTTAT GGAATCCTGC AAAGTGATGC CTCAGGTAAG TGAATGGCTT	180
TTGACAATGT ATTAAAATGC AAGTCATGCG TAGGGTAATG AGTCCACTCT TCCTGAAAAT	240
GAATTTAAAT AAACATAATG TTATTCATGT CCATTGTCTT CTGCGGTANA ANATNAATCA	300
TAAAGCAGAA TAATAGAATT TTGATGATGG GAAAGAACCA TTGCTGTCTC TAGTCTTCAT	360
GGGGATAGGA GTACACAGGG GGCAGTGGGG CCGCTGTGTT TTAAACACAG GTATTTTCC	420
NTACCTTCAC ATTCAAGCAA CTAGGATATT TGCTTTTCC CTTACCTCAG TCCCTTGGGG	480
GAAAAT	486

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAATGATCAT GTGGTCTATG AGAAAGAACCC AGGANAGGAG CTACTCATTC CCTGTACGGT	60
TATTTTAGTT TTCTGATGGA TTCTCGCAAT GAGGTTTGGT GGACCATTGA TGGANAAAAA	120
CCTGATGACA TCACTATTNG ATTGTCAACA TTTAACNGA	159

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCCATGA CACTTCTGTG GTGTG	25
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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCGACTCAC TGACCGCATC T

21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATCCATCC GCCATCATGA CACTTCTGTG GTGTG

35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCTAGAAAAG CGTAGTCTGG GACGTCGTAT GGGTACTGAC CGCATCT

47

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACTGGATCC GCCATCATGA CACTTCTGTG GTGTG

35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCCTCA CTGACCGCAT CT

22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GACTGGATCC GCCATCATGA CACTTCTGTG GTGTG

35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTGGTACC CATAGAAATC ATGTGTATAAC C

31